Johns Hopkins University

Department of Biology Seminar Series

Thursdays, 4:00pm

For more information go to:
https://bio.jhu.edu/events

Mudd Room 100 - November 14th, 2024

Shawn Burgess

Co-Deputy Director
Senior Investigator
Head
Chief

Developmental Genomics
Section
National Human Genome
Research Institute

National Institutes of Health

Host: Erin Jimenez

Darwinian Genomics: Rapid advances in genome assembly can make any fish a model organism

Fish are, by far, the most diverse group within the vertebrate lineage with extreme variations in physiology, morphology, and niche adaptation. For the study of evolutionary biology, developmental biology, physiology, population genetics, and many other disciplines, this vast collection of organisms represents an incredible opportunity, limited somewhat in the past by our ability to generate sufficient genomic information on a scale that would make these questions tractable. These limits historically are the reason why researchers focused on a small number of "model organisms" that were easy and inexpensive to raise in captivity. Resources were pooled to generate the needed genomic information which involved complex integration of DNA sequencing and incomplete mRNA data. In the past decade, new sequencing technologies, molecular biology techniques, and computational approaches have radically changed what is possible with a relatively "modest" investment in personnel and equipment when it comes to genome assembly and building gene models. I will give three examples of fish genome assembly, how the technologies have improved between each one, what kinds of data can be extracted by picking a specific fish model, and what the current state-of-the-art is for quickly generating new genomic data for a species of interest.